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SUMMARIES

Result No.	Score	Query Match Length	DB	ID	Description
1	1002	100.0	1097	22	ABA08605 Human LAK-4p homolog
2	1002	100.0	1097	22	AAK53221 Human polynucleotide
3	1002	100.0	1219	22	AAF82463 Human CASB411-rel
4	1002	100.0	1312	22	AAK52237 Human polynucleotide
5	1002	100.0	1461	21	AAA78402 Human secreted protein
6	1002	100.0	1813	22	AAH18131 Human CDNA sequence
7	1002	100.0	1960	22	AAF82462 Human CASB6411-rel
8	1002	100.0	2243	21	AAA64684 cDNA encoding a human gene
9	1002	100.0	2407	22	AAF82460 Human CASB6411-CDN
10	1002	100.0	2521	22	AAF82461 Alternatively spliced human gene
11	953	95.1	1194	23	ABV25683 Human prostate exp
12	953	95.1	1194	23	ABV28278 Human prostate exp
13	953	95.1	1194	23	ABV28278 Human prostate exp
14	620	61.9	470	22	AAL18591 Human breast cancer
15	614	61.3	501	22	AAL09919 Human breast cancer
16	391.5	39.1	777	22	AAH08034 Human CDNA clone
17	391	39.0	617	23	ABV12915 Human prostate exp
c	18	387	38.6	286	ABV08852 Human prostate exp
19	315	31.4	233	22	AAL10187 Human breast cancer
20	306	30.5	197	22	AAL19767 Human breast cancer
21	293	29.2	2902	24	ABQ54905 Human ovarian anti-progestin receptor
22	285	28.4	590	23	ABV34041 Human prostate exp
23	285	28.4	590	23	ABV42908 Human prostate exp
24	266	26.5	555	22	AAL20351 Human breast cancer
25	212	21.2	402	22	AAF65737 Novel human polynucleotide
26	177	17.7	454	22	ABA58847 Human foetal liver
27	177	17.7	454	22	AAK0704 Human brain expression
28	177	17.7	454	22	AAK32745 Human bone marrow probe
29	177	17.7	454	22	AAI38558 #7244 used t
30	177	17.7	454	24	ABO7543 Human genome-derived
31	172	17.2	498	22	AAL11452 Human breast cancer
32	157	15.7	523	23	ABV03746 Human prostate expression
33	148	14.8	94	22	ABA71379 Human foetal liver
34	148	14.8	94	22	AAK19696 Human brain expression
35	148	14.8	94	22	AAK45716 Human bone marrow
36	148	14.8	94	22	AAI151641 Probe #20327 used
37	148	14.8	94	24	ABSI1993 Human genome-derived
38	124.5	12.4	545	20	AAX20418 Human secreted protein
39	107.5	10.7	1633	22	AAS21352 Human cDNA sequence
40	104.5	10.4	2703	22	AAK94324 Human full-length
41	104.5	10.4	6391	22	AAL26423 Human breast cancer
42	101.5	10.1	5929	23	ABL05865 Drosophila melanogaster gene
43	97	9.7	5027	23	AAS92296 DNA encoding novel
44	93.5	9.3	1442	20	AAX13617 Enterococcus faecalis
45	9.1	9.1	486	22	AHH84071 Pongo pygmaeus olfactory receptor gene

ALIGNMENTS					
RESULT 1					
1	ABA08605	ABA08605 standard; cDNA; 1097 BP.	ID	ABA08605	Human LAK-4p homologue-encoding cDNA, SEQ ID NO:381.
2	XX	XX	XX	XX	Human LAK-4p homologue-encoding cDNA, SEQ ID NO:381.
3	AC	ABA08605;	DT	11-JAN-2002	(first entry)
4	DE				
5	KW	Human; cytokine; cell proliferation; cell differentiation; growth factor; hematopoiesis regulation; tissue growth; immunomodulator; activin; inhibitor; chemotaxis; thrombolytic; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder;			
6	KW				
7	KW				
8	KW				
9	KW				
10	KW				
11	KW				
12	KW				
13	KW				
14	KW				
15	KW				
16	KW				
17	KW				
18	KW				
19	KW				
20	KW				
21	KW				
22	KW				
23	KW				
24	KW				

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiallergic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropics; cardiotonic; virucide; antibacterial; antifungal; vulnerary; antiulcer; ss.

XX Homo sapiens.

XX WO200157188-A2.

PD 09 AUG-2001.

XX 05-FEB-2001; 2001WO-US03800.

PR 03-FEB-2000; 2000US-0496914.

PR 27-APR-2000; 2000US-0560875.

XX (HYSE-) HYSEQ INC.

PR Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-457740/49.

DR P-PSDB; ABB11361.

XX Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -

PS Claim 1; Page 473; 1963pp; English.

XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; haemopoiesis regulatory activity; tissue growth activity; immunomodulatory activity; chemotactic or chemokinetic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis. Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. Polypeptides with growth factor activity may be used in cell cultures to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a novel human polypeptide of the invention.

SQ Sequence 1097 BP; 288 A; 246 C; 247 G; 316 T; 0 other;

* Alignment Scores: 1.69e-108 Length: 1097 Score: 1002.00

	Percent Similarity:	Conservative:
	Best Local Similarity:	Mismatches:
	Query Match:	Indels:
DB:	22	Gaps:
US-09-895-298A-83 (1-190) x ABA08605 (1-1097)		
QY 1 MetMetAsnPheGlnProProSerLysAlaLrpArgAlaSerGlnMetMetThrPhephe	20	
Db 269 ATGATGAAATTCCAGCCTCGAGCAAAGCCTGGGGGCTCACAGATGATGACTTCTTC	328	
QY 21 IlePheIleLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaLeThrile	40	
Db 329 ATCTCTTGCTCTTTCACCTCACCTTCACGGGCTTGACCCATCACCATC	388	
QY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis	60	
Db 389 TGGAGATTAAGCTTCATGGAACTCTCATGGAAAGTGTGCACTTCTTCATTCAC	448	
QY 61 SerIleThrSerTripleaspthrLeuSerThrArgProGlyTyrlLeutRpvalValTrp	80	
Db 449 TCCATCTACAGCTGATCGACACCCATAAGTACACGGCTGGTACCTGGGGTGTGTTGG	568	
QY 81 IleIleArgAsnLeuIleIleGlySerValHisPhePhePhePheIleIleLeuIleValle	100	
Db 509 ATCTATCGGAACCTCATGGAAAGTGTGCACTTCTTCATCCTCACCATGGCT	568	
QY 101 IleIleThrThrLeuTyrrpglnIleIleGluGlyArgGlyIleMetIleArgLeuLeu	120	
Db 569 ATCATTACCTATCTTACTGGCAGATCACAGAGGAAGGAAGGAGATTATGATAAGGCTGCTC	628	
QY 121 HisGluGlnIleIleAsnGluGlyLysAspLysMetPheIleIleGluIleLeuIleLys	140	
Db 629 CATGAGCAGATCATATAGGGCAAGATAATGTCCTGATGAAATTGATCAG	688	
QY 141 LeuGlnAspMetGluLysIysAlaAsnProserSerLeuValleGluIargArgGluVal	160	
Db 689 CTGCAGGATATGGGAAGAAAGCAAACCCCAGCTCACTGCTCTGGAAAGGAGGGTG	748	
QY 161 GluGlnGlnGlyPheLeuHisIleGlyGluHisAspGlySerLeuAspLeuArgSerArg	180	
Db 749 GAGCAACAAGGCTTTCATGCTGGGAACATGATGGCACTGCTGACTTGCGATCTAGA	808	
QY 181 ArgSerValGlnGluGlyAsnProArgAla 190		
Db 809 AGATCAGTTCAAGAAGGTAATCCAAAGGCC 838		
RESULT 2		
AAK53221		
ID AAK53221 standard; cDNA; 1097 BP.		
XX		
AC AAK53221;		
XX		
DT 06-NOV-2001 (first entry)		
XX		
DE Human polynucleotide SEQ ID NO 2750.		
XX		
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haemopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.		
XX		
OS Homo sapiens.		
XX		
PN WO200157190-A2.		
XX		
PD 09-AUG-2001.		
XX		
PF 05-FEB-2001; 2001WO-US04098.		
XX		
PR 03-FEB-2000; 2000US-0496914.		
PR 27-APR-2000; 2000US-0560875.		
PR 20-JUN-2000; 2000US-0598075.		

PR 19-JUL-2000; 2000US-0620325.
 PR 01-SEP-2000; 2000US-0654936.
 PR 15-SEP-2000; 2000US-0663561.
 PR 20-OCT-2000; 2000US-0693325.
 PR 30-NOV-2000; 2000US-0728422.
 XX
 PA (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
 PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Weijerman T, Goodrich R;
 XX WPI; 2001-476283/51.
 DR P-PSDB; AAM8088.
 XX PT Nucleic acids encoding polypeptides with cytokine-like activities,
 PS useful in diagnosis and gene therapy.
 XX
 Claim 1; Page 4962; 6221pp; English.

CC The invention relates to poly nucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAK78323-AAM80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC poly nucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haemato poiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 (AAM8020) are omitted as the relevant pages from the sequence listing
 XX were missing at the time of publication.

SQ Sequence 1097 BP; 288 A; 246 C; 247 G; 316 T; 0 other;

Alignment Scores:

Pred. No. :	1.69e-108	Length:	1097
Score:	1002.00	Matches:	190
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	22	Gaps:	0

US-09-895-298A-83 (1-190) x AAK53221 (1-1097)

QY 1 MetMetAsnPheGlnProProSerLysAlaTrpArgAlaSerGlnMetMetThrPhePhe
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 269 ATGATGAATTCCAGGCCCTGGCAAAGCCTGGGGCCACAGATGACTTTCTTC 328

QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysthrLeuAlaLeuThrIle 40
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 329 ATCTTCTGCTCTTTCACCGGGCTTGACCCATCACCATC 388

QY 41 TrpArgLeuLysProSerAlaLysCysGlyProPheArgGlyLeuProLeuPheIleHis 60
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 389 TGGAGATGAAGCCTCACTGACTGTGGCCCTTTGAGGCGCTCTTCATTCAC 448

QY 61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrp 80
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 449 TCCATCTACAGCTGGATGACACCCATAAGTACACGGCTGSGTACCTGGGGTTGG 508

QY 81 IleTyrArgAsnLeuIleGlySerValHisPhePheIleLeuThrIleLeuValLeu 100
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 509 ATCTATCGGAACTCATGGAGTGTGCACTTCTTTCATCCACCCCTCATGGCTA 568

QY 101 IleLeuThrTyrLeuIleTyrTrpGlnIleThrGluGlyArgIleLysIleMetIleArgLeuLeu 120
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 569 ATCATCACCTATCTTACTGGCAGATCACAGAGGAAGGAGATATGATAAGGTGCTC 628

QY 121 HisGluGlnIleLeuAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140
 ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 629 CATGAGCAGATCATTAAATGAGGGCAAAGATAATGTTCTGATAGAAAATGATCAAG 688
 QY 141 LeuGlnAspMetGluLysIysAlaAsnProSerSerLeuValLeuGluGargGluVal 160
 Db 689 CTGCAGGATATGGAGAAGAAAGCAAACCCCAGCTCACTGTCTGGAAAGGAGAGGTG 748
 QY 161 GluGlnGlnGlyPheLeuHisLeuGlyGluHisAspGlySerLeuAspIeuArgSerArg 180
 Db 749 GAGCAACAAGGCTTTGCAATTGGGGACATGATGATGGCAGCTTGACTTGCGATCTAGA 808
 QY 181 ArgSerValGlnGluGlyAsnProArgAla 190
 Db 809 AGATCAGTTCAGAGGTAATCCAAGGGCC 838

RESULT 3
 AAF82463
 ID AAF82463 standard; cDNA; 1219 BP.
 XX
 AC AAF82463;
 XX
 DT 29-JUN-2001 (first entry)
 XX
 DE Human CASB6411-related cDNA #2.
 XX
 KW Human; CASB6411; vaccine; gene therapy; immunoprophylaxis;
 KW ovarian cancer; colon cancer; autoimmune disease; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..576
 FT /*tag= a /partial
 FT /note= "this sequence does not contain a start codon"
 XX
 PN WO200123417-A2.
 XX
 PD 05-APR-2001.
 XX
 PF 27-SEP-2000; 2000WO-EP09500.
 XX
 PR 30-SEP-1999; 99GB-0023154.
 PR 07-JUL-2000; 2000GB-0016839.
 XX
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX
 PI Vinals De Bassols YC;
 XX
 DR WPI; 2001-316133/33.
 DB P-PSDB; AAB83082.

XX
 PT Novel CASB6411 polypeptides useful in diagnostics, and as vaccines for
 PT prophylactic and therapeutic treatment of cancers, particularly ovarian
 and colon cancers, autoimmune diseases and related conditions -
 XX
 PS Claim 32; Page 66-67; 95pp; English.

CC The present sequence is provided in a specification relating
 to CASB6411 polypeptides comprising a sequence having at least 70%
 identity to a sequence of 460 or 154 amino acids fully defined in
 the specification. CASB6411 polypeptides and poly nucleotides are
 useful for treating a subject by immunoprophylaxis or therapy.
 The CASB6411 polypeptides are useful in diagnostics, and as
 vaccines for prophylactic and therapeutic treatment of cancers,
 particularly ovarian and colon cancers, autoimmune diseases and related
 conditions. CASB6411 polypeptides are also useful for the
 structure-based design of agonists, antagonists or inhibitors of the
 polypeptide.

XX
 SQ Sequence 1219 BP; 346 A; 260 C; 275 G; 338 T; 0 other;
 Pred. No. : 1.97e-108 Length: 1219

Score: 1002.00 Matches: 190
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 22 Indels: 0
 DB: 22 Gaps: 0

US-09-895-298A-83 (1-190) x AAF82463 (1-1219)

QY 1 MetMetAsnPheGlnProProSerLysAlaTrpArgAlaSerGlnMetMetThrPhePhe 20
 PR 19-JUL-2000; 2000US-0598075.
 PR 01-SEP-2000; 2000US-0620325.
 PR 15-SEP-2000; 2000US-0663561.
 PR 20-OCT-2000; 2000US-0693325.
 PR 30-NOV-2000; 2000US-0728422.

DB 64 ATCTCTTGCTCTTTCACCGGGCTTGTGCACCTGGCCATCACCAC 123
 PR PA (HYSE-) HYSEQ INC.

QY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPheIleHis 60
 PR XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
 PR 4 ATGATGAATTCCAGCCCTCCGAGCAAGCCTGGGGCTCACAGATGATGACTTTCTC 63
 PR PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PR PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;

QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlaLeuThrIle 40
 PR XX DR WPI; 2001-476283/51.
 PR DR P-PSDB; AAM79104.

DB 124 TGGAGATGAAAGCCTTCAGCTGACTGGCCCTTTCAGGAGCTCTCTCATCAC 183
 PR XX PS Claim 1; Page 2615-2616; 6221pp; English.

QY 61 SerIleTyRSerTrpIleAspThrLeuSerThrArgProGlyTyRLeuTrpValValTrp 80
 PR XX CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 PR encoded polypeptides (AAM8323-AAM80302) that exhibit activity relating to
 PR cytokine, cell proliferation or cell differentiation or which may induce
 PR production of other cytokines in other cell populations. The
 PR polynucleotides and polypeptides are useful in gene therapy, vaccines or
 PR peptide therapy. The polypeptides have various cytokine-like activities,
 PR e.g., stem cell growth factor activity, haemopoiesis regulating
 PR activity, tissue growth factor activity, immunomodulatory activity and
 PR activin/inhibin activity and may be useful in the diagnosis and/or
 PR treatment of cancer, leukaemia, nervous system disorders, arthritis and
 PR inflammation.
 PR Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 PR (AAW8020) are omitted as the relevant pages from the sequence listing
 PR were missing at the time of publication.

Db 364 CATGAGCAGATCATATAATGAGGCCAAGATAAAATGTCTCTGATAGAAATGATCAAG 423
 PR CC SQ Sequence 1312 BP; 370 A; 286 C; 287 G; 369 T; 0 other;

QY 141 LeuGlnAspMetGluIleLysAlaAsnProSerSerLeuValLeuGluIgarginGluVal 160
 PR CC SQ Alignment Scores:
 PR Pred. No.: 2.19e-108 Length: 1312
 PR Score: 1002.00 Matches: 190
 PR Percent Similarity: 100.00% Conservative: 0
 PR Best Local Similarity: 100.00% Mismatches: 0
 PR Query Match: 22 Indels: 0
 PR DB: 22 Gaps: 0

DB 424 CTGCAGGATATGGAGAGAAAGCMACCCCAGCTCACTTGTCTGGAAAGGAGAGGTG 483
 PR CC SQ US-09-895-298A-83 (1-190) x AAK52237 (1-1312)

QY 161 GluGlnGlnGlyPheLeuHisLeuGlyGluHisAspGlySerLeuAspLeuArgSerArg 180
 PR DB 294 GAGCAAACAAGCTTTGCAATTGGGGAACATGATGGCAGCTTGACTTGCGATCTAGA 543
 PR CC SQ QY 181 ArgSerValGlnGluGlyAsnProArgAla 190
 PR DB 544 AGATCAGTCAAGAGGTAATCCAAAGGCC 573
 PR CC SQ

RESULT 4
 AAK52237
 ID AAK52237 standard; cDNA; 1312 BP.

XX AAK52237;
 XX DT 06-NOV-2001 (first entry)
 DE Human polynucleotide SEQ ID NO 782.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 tissue growth factor; immunomodulatory; cancer; leukaemia;
 nervous system disorder; arthritis; inflammation; ss.

XX OS Homo sapiens.
 XX WO200157190-A2.

PD 09-AUG-2001.

XX 05-FEB-2001; 2001WO-US04098.

XX 03-FEB-2000; 2000US-0496914.

PR 27-APR-2000; 2000US-0560875.

QY 81 IleTyRArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuLeuValLeu 100
 PR DB 534 ATCTATCGGAACCTCATGGAAAGTGCTGCACTCTTTCTCATCCTCACCCATCTGCTA 593
 PR QY 101 IleLeuThrTyRLeuTyrrpGlnIleIleGluGlyArgLysIleMetIleArgLeuLeu 120
 PR DB 594 ATCATACTTACTGGCAGATCACAGAGGAAGGAGATTAGATAAGGCTGCTC 653
 PR QY 121 HisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleIle 140

PF 28-JUL-2000; 2000EP-0116126.
 XX
 PR 29-JUL-1999; 99JP-0248036.
 PR 27-AUG-1999; 99JP-0300253.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PT Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX
 WPI; 2001-318749/34.

PR Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
 XX
 PS claim 8; SEQ ID 18001; 2537pp + CD ROM; English.
 XX
 CC The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAB95893 to AAH18742 represent human cDNA sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.
 XX
 Sequence 1813 BP; 489 A; 400 C; 405 G; 519 T; 0 other;

SQ Alignment Scores:
 Pred. No.: 3 5e-108 Length: 1813
 Score: 1002.00 Matches: 190
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: DB: 22 Indels: 0
 Gaps: 0
 US-09-895-298A-83 (1-190) x AAH18131 (1-1813)

QY 1 MetMetAsnPheGlnProProSerIysAlaTrpArgAlaSerGlnInMetMetThrPhePhe 20
 |||||ATGATGAATTCCAGCTCCAGACAAGCCTGGGGCTCACAGATGATGACTTC 510

DB 451 ATGATGAATTCCAGCTCCAGACAAGCCTGGGGCTCACAGATGATGACTTC 510

QY 21 IlePheLeuPhePheProSerPheThrGlyValLeuCystThrLeuAlaLleThrIle 40
 |||||ATCTCTTGCTCTTTCACGGGGCTGCGACCTGGCATCACCAC 570

QY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyIleuProLeuPheLeuHis 60
 |||||ATGGAGATTGAAAGCCTTCAGCTGACTGTGGCCTTTGAGGTCTGGCTCTTCATTCAC 630

QY 61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrp 80
 |||||TCCATCTACAGCTGGATCACACGCCCTGGCTACCTGTGGTTGG 690

Db 751 ATCATCACCTATCTTACGGCATCACAGAGGAAGATATGATAAGGCTGCTC 810

QY 121 HisGluGlnIleLeuAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140
 |||||CATGAGCAGATCATTAATGAGGGCAAGATAAAATGTTCTGTATAGAAAATTGATCAAG 870

Db 871 CTGCAGGATATGGAGAAGAACCAAACCCAGCTACTGCTCTGGAAAGGAGGGTG 930

QY 161 GluGlnGlnGlyPheLeuHisLeuGlyGluHisAspGlySerLeuAspLeuArgSerArg 180
 |||||GAGCAACAAAGGCTTGTGCAATTGGGGAAACATGATGGCACTTGACCTTGACATCTAGA 990

QY 181 ArgSerValGlnGluGlyAsnProArgAla 190
 |||||AGATCAGTTCAAGAAGGTAAATCCAAGGCC 1020

Db 991 RESULT 7
 AAF82462
 ID AAF82462 standard; cDNA; 1960 BP.
 XX
 AC AAF82462;
 DT 29-JUN-2001 (first entry)
 XX
 DE Human CASB6411-related cDNA #1.
 XX
 KW Human; CASB6411; vaccine; gene therapy; immunoprophylaxis;
 KW ovarian cancer; colon cancer; autoimmune disease; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1317
 FT /*tag= a
 FT /partial
 FT /*note= "this sequence does not contain a start codon"
 XX
 PN WO200123417-A2.
 XX
 PD 05-APR-2001.
 XX
 PF 27-SEP-2000; 2000WO-EP09500.
 XX
 PR 30-SEP-1999; 99GB-0023154.
 PR 07-JUL-2000; 2000GB-0016839.
 XX
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX
 PI Vinals De Bassols YC;
 XX
 DR WPI; 2001-316133/33.
 DR P-PSDB; AAB83081.

PT Novel CASB6411 polypeptides useful in diagnostics, and as vaccines for prophylactic and therapeutic treatment of cancers, particularly ovarian and colon cancers, autoimmune diseases and related conditions -
 XX
 PS Claim 32; Page 65-66; 95pp; English.
 XX
 CC The present sequence is provided in a specification relating to CASB6411 polypeptides comprising a sequence having at least 70% identity to a sequence of 460 or 154 amino acids fully defined in the specification. CASB6411 polypeptides and polynucleotides are useful for treating a subject by immunoprophylaxis or therapy.
 CC The CASB6411 polypeptides are useful in diagnostics, and as

Db 760 ATCTTCTTGCTCTTCCCACCTTCACGGGGCTTGTGCACCCGGCATCAC 819
QY 41 TrpArgLeuLysProSerAlaaspCysGlyProPheArgGlyLeuProLeuPheLeuHis 60
Db 820 TCGAGATGGAAGCCTTCAGCTGACTGGCCCTTTCAGGTCAGCTCTTCATC 879
QY 61 SerIleTySerTrpIleAspThrLeuSerThrArgProGlyTyreLeuTrpValValTrp 80
Db 880 TCCAACTACAGCTGGATCGACACCCAAAGTACACGGCCTGGCTACGGGGTTGG 939
QY 81 IleTyArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuValLeu 100
Db 940 ATCTATCGAACCTCATGGAAAGTGTGCACTCTTTCATCCACCCATGGCTA 999
QY 101 IleIleThrTyLeuTrpRglnIleIleGlyArglyArglyIleMetIleArgLeu 120
Db 1000 ATCATCACCTACTTACTGGCAGCACAGAGGAAGGATATTGATAAGGCTGTC 1059
QY 121 HisGluglnIleIleAsnGluGlyAspLysMetPheLeuIleGluLysLeuIleLys 140
Db 1060 CATGAGCAGATCATTATGAGGCCAAGATAAAATGTTCTGTAGAAAATTGATCAA 1119
QY 141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgArgGluVal 160
Db 1120 CTGCAGGATATGGAGAGAAAGCAACCCAGCTCACTGTCTGGAAAGGAGAGGTG 1179
QY 161 GluGlnGlnGlyPheLeuHisLeuGlyGluHisAspGlySerLeuAspLeuArgSerArg 180
Db 1180 GAGCAACAGGCTTTGCAATTGGGGAACATGATGGCAGCTGACTTGCGATCTGAG 1239
QY 181 ArgSerValGlnGluGlyAsnProArgAla 190
Db 1240 AGATCAGTTCAAGAAGGTAAATCCAAAGGCC 1269
RESULT 9
AAF82460
ID AAF82460 standard; cDNA; 2407 BP.
XX AAC82460;
XX 29-JUN-2001 (first entry)
DE Human CASH6411 cDNA.
XX Human; CASH6411; vaccine; gene therapy; immunoprophylaxis;
KW ovarian cancer; colon cancer; autoimmune disease; ss.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 382..1764
FT /*tag= a /product= "CASH6411"
XX WO200123417-A2.
PD 05-APR-2001.
PF 27-SEP-2000; 2000WO-EP09500.
XX 30-SEP-1999; 99GB-0023154.
PR 07-JUL-2000; 2000GB-0016839.
XX (SMK) SMITHKLINE BECHAM BIOLOGICALS.
PA Vinals De Bassols YC;
XX WPI; 2001-316133/33.
DR P-PSDB; AAB83079.
XX Novel CASB6411 polypeptides useful in diagnostics, and as vaccines for prophylactic and therapeutic treatment of cancers, particularly ovarian and colon cancers, autoimmune diseases and related conditions -
PT

xx PS Claim 11; Page 63-64; 95pp; English.
xx The present sequence encodes human CASH6411 polypeptide. The invention relates to CASH6411 polypeptides comprising a sequence having at least 70% identity to a sequence of 460 or 154 amino acids fully defined in the specification. CASH6411 polypeptides and poly nucleotides are useful for treating a subject by immunoprophylaxis or therapy. The CASH6411 polypeptides are useful in diagnostics, and as vaccines for prophylactic and therapeutic treatment of cancers, particularly ovarian and colon cancers, autoimmune diseases and related conditions. CASH6411 polypeptides are also useful for the structure-based design of agonists, antagonists or inhibitors of the polypeptide. The present sequence may be alternatively spliced to generate a sequence encoding a truncated CASH6411 protein.
cc CC
sq Sequence 2407 BP; 635 A; 557 C; 546 G; 669 T; 0 other;

Alignment Scores:
pred. No.: 5.26e-108 Length: 2407
Score: 1002.00 Matches: 190
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-895-298A-83 (1-190) x AAF82460 (1-2407)

QY 1 MetMetAsnPheGlnProProSerLysAlaTrpPARGAlaSerGlnMetMetThrPhePhe 20
Db 1192 ATGATGAAATTCCAGCTCCGACCAAAGCCTGGGGGCTCACAGATGACTTTCTC 1251
QY 21 IlePheLeuPhePheProSerPhethRglyValLeuCysThrLeuAlarlethrile 40
Db 1252 ATCTTCTTGCTCTTTCACCTCTCACGGGCTTGTGCACCCGGCATCACCATC 1311
QY 41 TrpArgLeuLysProSerAlaaspCysGlyProPheArgGlyLeuProLeuPheLeuHis 60
Db 1312 TCGAGATGGAAGCCTTCAGCTGACTGGAACTCTCATCCACCCATGGCTA 1371
QY 61 SerIleTySerTrpIleAspThrLeuSerThrArgProGlyTyreLeuTrpValValTrp 80
Db 1372 TCCATCTACAGCTGATCGACACCTTAAGTACACGGCCTGGCTACGGT 1431
QY 81 IleTyArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuValLeu 100
Db 1432 ATCTATCGAACCTCATGGAACTCTCATCCACCCATGGCTA 1491
QY 101 IleIleThrTyLeuTrpRglnIleIleGlyArglyArglyIleMetIleArgLeu 120
Db 1492 ATCATCACCTATCTTACTGGCAGATCACAGTGTGCACTCTTCCATCCACCCATGGCTA 1551
QY 121 HisGluglnIleIleAsnGluGlyAspLysMetPheLeuIleGluLysLeuIleLys 140
Db 1552 CATGAGCAGATCATTATGAGGCCAAGATAAAATGTTCTGTAGAAAATTGATCAA 1611
QY 141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgArgGluVal 160
Db 1612 CTGCAGGATATGGAGAGAAAGCAACCCAGCTCACTGTGTCAGCTGGCTACGGGGTTGG 1671
QY 161 GluGlnGlnGlyPheLeuHisLeuGlyGluHisAspGlySerLeuAspLeuArgSerArg 180
Db 1672 GAGCAACAAAGGCTTGTGCAATTGGGGAACTATGATGGCAGCTGACTTGCGATCTGAG 1731
QY 181 ArgSerValGlnGluGlyAsnProArgAla 190
Db 1732 AGATCAGTTCAAGAAGGTAAATCCAAAGGCC 1761
RESULT 10
AAF82461
ID AAF82461 standard; cDNA; 2521 BP.
XX
AC AAF82461;

XX DT 29-JUN-2001 (first entry) Db 1426 TGGAGGATGAAGCCTTCAGCTGACTGTGCCCTTCGAGGTCGCCCTCTCATTCAC 1485
 XX DE Alternatively spliced human CASB6411 cDNA encoding truncated protein. QY 61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrp 80
 XX KW Human; CASB6411; vaccine; gene therapy; immunoprophylaxis; 1486 TCCATCTACAGCTGGATCACCCCTAAGTACACGGCTGGCTACCTGGGGTTGG 1545
 KW ovarian cancer; colon cancer; autoimmune disease; isoform; alternative splicing; ss.
 XX OS Homo sapiens. QY 81 IleTyArgAsnLeuIleGlySerValHisPhephepheleuthLeuIleValLeu 100
 XX FH Location/Qualifiers 1546 ATCTATCGAACCTCATGGAAAGTGTGCACCTCTTTCATCCTCACCCCTCATTGTC 1605
 XX CDS 382. 846 /tag= a Db 1606 ATCATCACCTATCTTACTGGAGATCACAGGGAAAGGAAGATTGATAAGGCTGCTC 1655
 XX FT /product= "truncated CASB6411" PN WO200123417-A2.
 XX PD 05-APR-2001. QY 121 HisGluGlnIleIleAsnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140
 XX PF 27-SEP-2000; 2000WO-EP09500. Db 1666 CATGAGCAGATCTTAATGAGGCCAAAGATAAAATGTCCTGATAGAAAATTGATCAAG 1725
 XX PR 30-SEP-1999; 99GB-0023154. QY 141 LeuGlnAspMetGluLysAlaAsnProSerSerIleValLeuGluArgArgGluVal 160
 XX PR 07-JUL-2000; 2000GB-0016839. Db 1726 CTGGAGGATATGGAGAGAACCAAACCCAGCTCACTTGCTCTGGAAAGGAGAGGTG 1785
 XX PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS. QY 161 GluGlnGlnGlyPheLeuHsIleuGlyGluHsAspGlySerIleAspLeuArgSerArg 180
 XX PI Vinals De Bassols YC; Db 1786 GAGCAACAAGGCTTTTGCAATTGGGGAAACATGATGGCAGCTTGACTGCGATCTAGA 1845
 XX DR WPI; 2001-316133/33. QY 181 ArgSerValGlnGluGlyAspProArgAla 190
 XX P-PSSB; AAB83080. Db 1846 AGATCAAGAAGGTAATCCAAGGGCC 1875
 XX PT Novel CASB6411 polypeptides useful in diagnostics, and as vaccines for prophylactic and therapeutic treatment of cancers, particularly ovarian and colon cancers, autoimmune diseases and related conditions PS Claim 11; Page 64-65; 95pp; English.
 XX PS The present sequence encodes a truncated CASB6411 polypeptide. It is generated by alternative splicing of the full length human cDNA sequence of CASB6411. The invention relates to CASB6411 polypeptides comprising a sequence having at least 70% identity to a sequence of 460 or 154 amino acids fully defined in the specification. CASB6411 polypeptides and polynucleotides are useful for treating a subject by immunoprophylaxis or therapy. The CASB6411 polypeptides are useful in diagnostics, and as vaccines for prophylactic and therapeutic treatment of cancers, particularly ovarian and colon cancers, autoimmune diseases and related conditions. CASB6411 polypeptides are also useful for the structure-based design of agonists, antagonists or inhibitors of the polypeptide. XX
 XX SQ Sequence 2521 BP; 662 A; 583 C; 583 G; 693 T; 0 other; RESULT 11 ABV22463
 XX Pred. No.: 5.62e-108 Length: 2521 ID ABV22463 standard; cDNA; 1194 BP.
 XX Score: 1002.00 Matches: 190 XX ABV22463;
 XX Percent Similarity: 100.00% Conservative: 0 XX DT 13-SEP-2002 (first entry)
 XX Best Local Similarity: 100.00% Mismatches: 0 DE Human prostate expression marker cDNA 22454.
 XX Query Match: 100.00% Indels: 0 KW Human; prostate cancer; cytostatic; carcinogen; pharmacogenomic marker; pharmacogenomic marker; gene; ss.
 XX DB: 22 Gaps: 0 OS Homo sapiens.
 XX WO200160860-A2. PN 200160860-A2.
 XX PD 23-AUG-2001. PR 20-FEB-2001; 2001WO-US05171.
 XX PR 17-FEB-2000; 2000US-183319P. PR 16-MAR-2000; 2000US-189862P.
 XX PR 25-MAY-2000; 2000US-207454P. PR 09-JUN-2000; 2000US-211314P.
 XX PR 18-JUL-2000; 2000US-219007P. PR 13-DEC-2000; 2000US-255281P.
 XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC. PA Schlegel R, Endege WO, Monahan JE;
 XX PI Schlegel R, Endege WO, Monahan JE;
 XX DR WPI; 2001-662795/76.
 XX QY 1 MetMetAsnPheGlnProProSerLysAlaTrpArgAlaSerGlnMetMetThrPhe 20 PT Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer PS Claim 1; Page 3912; 11750pp; English.
 XX Db 1306 ATGATGAAATTCCAGCCICGGAAAGCCTGCGGGCCTCACAGATGACTTCTTC 1365 PT The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for:
 CC

CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate
 CC cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
 CC in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a
 CC patient;
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX Sequence 1194 BP; 288 A; 287 C; 278 G; 339 T; 2 other;

Alignment Scores:
 Pred. No.: 1.19e-102 Length: 1194
 Score: 953.00 Matches: 186
 Percent Similarity: 97.89% Conservative: 0
 Best Local Similarity: 97.89% Mismatches: 4
 Query Match: 95.11% Indexes: 1
 DB: 23 Gaps: 0

US-09-895-298A-83 (1-190) x ABV22463 (1-1194)

QY 1 MetMetAsnPheGlnProProSerLysAlaTrpArgAlaSerGlnMetMetThrPhePhe 20
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 531 ATGATGAATTCCAGCCTCGAGCAAAGCCTGGGGCTCACAGATGACTTCTC 590
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlleThrIle 40
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 591 ATCTCTTGCTCTTTCCCATCTTCACCGGGTCTGTGCACCTGGCCATCACCATC 650
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPhenIle 60
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 651 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTCGAGGTCAGCCTCTTCATTAC 710
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 61 SerIleTyrSerTriPheAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrp 80
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 711 TCCATCTCACAGCTGGATCGACACCTTAAGTACACGGCTGGCTACCTGGTTGG 770
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 81 IleTyrArgAsnLeuIleGlySerValHisPhePheIleLeuThrLeuIleValLeu 100
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 771 ATCTATGGAACTCTCATTTGAGACTCTTTCATCCCTACCTCATGGCTA 830
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 101 IleLeuThrTyrLeuTyrrPheIleLeuIleLeuLeuLeuLeuLeuLeuLeuLeu 120
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 831 ATCATCACTATCTTACTGGCAGTACAGAGGGAAAGGAAGGATATGATAAGGCTGTC 890
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 121 HisGluGlnIleLeuAspGlyLysAspLysMetPheLeuIleGluLysLeuLeuLys 140
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 891 CATGAGCGAGATCATTAATGAGGCCAAGATAAAATGTTCTCTGATAGAAAATGATCAAG 950
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValLeuGluArgGluVal 160
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 951 CTGCAGGATATGGAGAAAGAACCCAGC-TCACTTGTAAGCAGGAAAGGAGAGGTG 1009
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 161 GluGlnGlnGlyPheLeuHisIleGluIyGluHisAspGlySerLeuAspLeuArgSerArg 180
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 1010 GAGCAACAAAGGTTATGGCATAGGGGACATGATGGCAGTCCTGACTTGGATCTAGA 1069
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 181 ArgSerValGlnGluGlyAsnProArgAla 190
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 1070 CGATCAGTCAAGAAGGTAATCCAAAGGCC 1099
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 12

ABV25683 ID ABV25683 standard; cDNA; 1194 BP.

XX AC ABV25683;

XX DT 16-SEP-2002 (first entry)

DE Human prostate expression marker cDNA 25674.
 XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 CC (h) pharmacogenomic marker; gene; ss.
 CC OS Homo sapiens.
 XX PN WO20010860-A2.
 XX PD 23-AUG-2001.
 XX PR 20-FEB-2001; 2001WO-US05171.
 XX PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-235281P.
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX PI Schlegel R, Endege WO, Monahan JE;
 XX DR WPI; 2001-662795/76.
 XX PT Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.
 XX PS Claim 1; Page 5146-5147; 11750pp; English.
 CC The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
 CC (a) assessing whether a patient is afflicted with prostate cancer;
 CC (b) monitoring the progression of prostate cancer in a patient;
 CC (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
 CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound;
 CC (g) determining whether prostate cancer has metastasized in a patient;
 CC (h) assessing the aggressiveness or indolence of prostate cancer in a patient;
 CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX Sequence 1194 BP; 288 A; 287 C; 278 G; 339 T; 2 other;

Alignment Scores:
 Pred. No.: 1.19e-102 Length: 1194
 Score: 953.00 Matches: 186
 Percent Similarity: 97.89% Conservative: 0
 Best Local Similarity: 97.89% Mismatches: 4
 Query Match: 95.11% Indexes: 1
 DB: 23 Gaps: 0

US-09-895-298A-83 (1-190) x ABV25683 (1-1194)

QY 1 MetMetAsnPheGlnProProSerLysAlaTrpArgAlaSerGlnMetMetThrPhePhe 20
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 531 ATGATGAATTCCAGCCTCGAGCAAAGCCTGGGGCTCACAGATGACTTCTC 590
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeuCysThrLeuAlleThrIle 40
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 591 ATCTCTTGCTCTTCCATCTCTTCACGGGGTCTGTGCACCTGGCCATCACCATC 650
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 41 TrpArgLeuLysProSerAlaAspCysGlyProPheArgGlyLeuProLeuPhenIle 60
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 651 TGGAGATTGAAGCCTTCAGCTGACTGTGGCCCTTTCGAGGAGCCTCTCATTCAC 710
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 61 SerIleTyrSerTriPheAspThrLeuSerThrArgProGlyTyrLeuTrpValValTrp 80

|||||||
Db 711 TCCATCTACAGCTGGATGACACCTTAAGTACACGGCTGGTACCTGGTTGGTGG 770
QY 81 IleTyrrArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuLeu 100
Db 771 ATCTATCGGAACCTCATGGAAAGTGTGCACTTCCTTCATCCTCACCCCTCATGGCTA 830
QY 101 IleIleThrTyrrLeuIleTrpGlnIleThrGluGlyArgLysIleMetIleArgLeuLeu 120
Db 831 ATCATCACCTATCTTACTGGCAGATCACAGAGGGAGGAGATTATGATAAGGCTGCRC 890
QY 121 HisGluGlnIleIleLeasnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140
Db 891 CATGAGCAGATCATTATGAGGGCAAAGATAAAATGTTCTGTAGATAAAAATTGATCAAG 950
QY 141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValleuAspLeuArgSerArg 160
Db 951 CTGCGAGGATATGGAGAGAAACCCAGC-TCACTGTACTGGAAAGGAGAGGTG 1009
QY 161 GluGlnGlnGlyPheLeuHisIleGluHisAspGlySerLeuValleuAspLeuArgSerArg 180
Db 1010 GAGCAACAAGGCTTATTCGATTAGGGAAACATGATGGCAGTGTGACTTGCGATCTAGA 1069
QY 181 ArgSerValGlnGluLysAsnProArgAla 190
Db 1070 CGATCAGTTCAAGAACGTAATCCAAGGCC 1099

RESULT 13

ID ABV28278 standard; cDNA; 1194 BP.
XX ABV28278;
XX DT 16-SEP-2002 (first entry)
DE Human prostate expression marker cDNA 28269.
XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX OS Homo sapiens.
PN WO20010860-A2.
XX PD 23-AUG-2001.
XX PF 20-FEB-2001; 2001WO-US05171.
XX PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PI Schlegel R, Endege WO, Monahan JE;
XX DR WPI; 2001-662795/76.

PT Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -
XX PS Claim 1; Page 5881-5882; 11750pp; English.

CC The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate

|||||||
Db 591 ATCTTCTGGCTCTTTCATCCCTCACCGGGGCTCTGCCACCTGGCCATCACCACTC 650
QY 41 TRPArgLeuLysProSerAlaAspCysGlyProPheIleArgGlyLeuProLeuPheLeuHis 60
Db 651 TGGAGATTGAAAGCCTTCAGCTGACTGTGGCCCTTTCGAGGCTGCCCCTCTTCATTCAC 710
QY 61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrrLeuTrpValValTrp 80
Db 711 TCCATCTACAGCTGGATGACACCTTAAGTACACGGCTACCTGGTTGGTGGTGG 770
QY 81 IleTyrrArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuLeu 100
Db 771 ATCTATCGGAACCTCATGGAAAGTGTGCACTTCCTTCATCCTCACCCCTCATGGCTA 830
QY 101 IleIleThrTyrrLeuIleTrpGlnIleThrGluGlyArgLysIleMetIleArgLeuLeu 120
Db 831 ATCATCACCTATCTTACTGGCAGATCACAGAGGGAGGAGATTATGATAAGGCTGCRC 890
QY 121 HisGluGlnIleIleLeasnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140
Db 891 CATGAGCAGATCATTATGAGGGCAAAGATAAAATGTTCTGTAGATAAAAATTGATCAAG 950
QY 141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValleuAspLeuArgSerArg 160
Db 951 CTGCGAGGATATGGAGAGAAACCCAGC-TCACTGTACTGGAAAGGAGAGGTG 1009
QY 161 GluGlnGlnGlyPheLeuHisIleGluHisAspGlySerLeuAspLeuArgSerArg 180
Db 1010 GAGCAACAAGGCTTATTCGATTAGGGAAACATGATGGCAGTGTGACTTGCGATCTAGA 1069
QY 181 ArgSerValGlnGluLysAsnProArgAla 190
Db 1070 CGATCAGTTCAAGAACGTAATCCAAGGCC 1099

|||||||
Db 1070 CGATCAGTTCAAGAACGTAATCCAAGGCC 1099

RESULT 14

ID AAL18591-
XX AC AAL18591;
XX DT 07-DEC-2001 (first entry)
XX DE Human breast cancer expressed polynucleotide 11048.
XX KW Human; breast cancer; cell marker; cytostatic; ss.

CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker;
CC Sequence 1194 BP; 288 A; 287 C; 278 G; 339 T; 2 other;
XX SQ Sequence 1194 BP; 288 A; 287 C; 278 G; 339 T; 2 other;

Alignment Scores:

Pred. No.:	1.19e-102
Score:	953.00
Percent Similarity:	97.89%
Best Local Similarity:	97.89%
Query Match:	95.11%
DB:	23
Gaps:	0

US-09-895-298A-83 (1-190) x ABV28278 (1-1194)

QY 1 MetMetAsnPheGlnProProSerLysAlaTrpPARCAlaSerGlnMetMetThrPhePhe 20
Db 531 ATGATGAATTCCACGCCCTCCGAGCAAAGCCTGGGGGCTCACAGATGATGACTTCCTRC 590
QY 21 IlePheLeuLeuPhePheProSerPheThrGlyValLeucysThrLeuAlaIleThrIle 40
Db 591 ATCTTCTGGCTCTTTCATCCCTCACCGGGGCTCTGCCACCTGGCCATCACCACTC 650
QY 41 TRPArgLeuLysProSerAlaAspCysGlyProPheIleArgGlyLeuProLeuPheLeuHis 60
Db 651 TGGAGATTGAAAGCCTTCAGCTGACTGTGGCCCTTTCGAGGCTGCCCCTCTTCATTCAC 710
QY 61 SerIleTyrSerTrpIleAspThrLeuSerThrArgProGlyTyrrLeuTrpValValTrp 80
Db 711 TCCATCTACAGCTGGATGACACCTTAAGTACACGGCTACCTGGTTGGTGGTGG 770
QY 81 IleTyrrArgAsnLeuIleGlySerValHisPhePhePheIleLeuThrLeuLeu 100
Db 771 ATCTATCGGAACCTCATGGAAAGTGTGCACTTCCTTCATCCTCACCCCTCATGGCTA 830
QY 101 IleIleThrTyrrLeuIleTrpGlnIleThrGluGlyArgLysIleMetIleArgLeuLeu 120
Db 831 ATCATCACCTATCTTACTGGCAGATCACAGAGGGAGGAGATTATGATAAGGCTGCRC 890
QY 121 HisGluGlnIleIleLeasnGluGlyLysAspLysMetPheLeuIleGluLysLeuIleLys 140
Db 891 CATGAGCAGATCATTATGAGGGCAAAGATAAAATGTTCTGTAGATAAAAATTGATCAAG 950
QY 141 LeuGlnAspMetGluLysLysAlaAsnProSerSerLeuValleuAspLeuArgSerArg 160
Db 951 CTGCGAGGATATGGAGAGAAACCCAGC-TCACTGTACTGGAAAGGAGAGGTG 1009
QY 161 GluGlnGlnGlyPheLeuHisIleGluHisAspGlySerLeuAspLeuArgSerArg 180
Db 1010 GAGCAACAAGGCTTATTCGATTAGGGAAACATGATGGCAGTGTGACTTGCGATCTAGA 1069
QY 181 ArgSerValGlnGluLysAsnProArgAla 190
Db 1070 CGATCAGTTCAAGAACGTAATCCAAGGCC 1099

Tue Nov 12 15:08:58 2002

us-09-895-298a-83.rng

Db	216	AAATGTTCTGTATAAGAAAATTGATCAAGCTGCCAGGATATTGGAAGAAAGCAACCCCC	275
Oy	151	SerSerLeuValLeuGluArgArgGluValGluGlnGlnGlyPheLeuHisLeuGlyGlu	170
Db	276	AGCTCACTTGTCTGAAAGGAGAGGGTGGAGCACAGGCTTTGCATTGGGGAA	335
Oy	171	HIS ASP GLY Ser Leu Asp Phe U Arg Ser Arg Arg Ser Val Gln Glu Gly Asn Pro Arg Ala	190
Db	336	CATGATGGCAGTCCTGACTTGCGATCTAGAANATCAGTCCAGAGGTAATCCAAGGCC	395

Search completed: November 9, 2002, 04:48:43
Job time : 303 secs

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